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Title:
Perfect score:
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                                                                                                                                                                                                                                                                            Minimum
Maximum
                                                                                                                                                                                              Database
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe:1
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
12: sp_vertebr:
13: sp_vertebr:
14: sp_unclass
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000 Com
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	σι	U	4	ω	N	ם	Result No.
117	117	119	127	131	134	140	143	143	145	152	152	152	247	247	291	291	298	301	Score
38.1	38.1	38.8	41.4	42.7	43.6	45.6	46.6			49.5				80.5	94.8	94.8	97.1	98.0	Query Match
298	280	208	438	224	597	281	197	195	264	501	501	496	610	324	589	589	602	1140	Length
4	4	12	G	11	11	12	13	13	12	11	11	11	13	13	11	H	11	4	B
09н2А8	о9нар7	055770	Q9VUX5	088642	Q9R015	8TNA60	Q91A69	Q91A70	Q9EN27	Q9EQ04	Q9EQ05	Q9ESF0	057319	Q9DDN2	Q9ESE8	090206	Q9ESE9	THND60	ij
Q9h2a8 homo sapien	Q9hap7 homo sapien	055770 chilo iride	Q9vux5 drosophila	088642 rattus norv	Q9r015 mus musculu	Q9yn18 choristoneu	Q9ia69 gallus gall	Q9ia70 gallus gall	Q9en27 amsacta moo	rattus	Q9eq05 rattus norv	Q9esf0 rattus norv	gallus	Q9ddn2 gallus gall	} rattus	Q9qzc6 rattus norv	Q9ese9 rattus norv	Q9unh1 homo sapien	Description

45	44	<u>4</u>	42	41	40	39	38	37	36	ω G	34	<u>ω</u>	32	31	30	29	28	27	26	25	24	23	22	21	20
65.5	68	69	69.5	71.5	72.5	73.5	77.5	82	83.5	84	84	86.5	87	88	90	92	100	101	103	103	105.5	106	107	111	113.5
21.3	22.1	22.5	22.6	23.3	23.6	23.9	25.2	26.7	27.2	27.4	27.4	28.2	28.3	28.7	29.3	30.0	32.6		33.6		34.4	34.5	34.9	36.2	37.0
234	428	250	4904	4845	142	137	284	155	187	87	87	292	285	87	281	301	268	268	261	150	276	377	379	313	153
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Q9YMP8	099GT7	Q99GY5	Q9VH01	088738	Q9GLN5	Q9BVZ4	Q9YKL5	61WA60	Q9DSW8	009120	009123	092394	60Ad60	009119	Q9DVT5	Q9PZ54	Q91F18	Q9E232	Q9QES9	Q9YVJ4	089744	Q9NJ07	Q9U492	Q9J827	Q9VEM2
	099gt7 heliocoverp	Q99gy5 heliocoverp	Q9vh01 drosophila	088738 mus musculu	Q9gln5 sus scrofa	Q9bvz4 homo sapien	09yk15 epiphyas po	Q9ymi9 lymantria d	Q9dsw8 ascovirus d	009120 mus musculu	009123 mus musculu	092394 bombyx mori	Q9pyq9 xestia c-ni	009119 mus musculu	Q9dvt5 plutella xy			Q9e232 helicoverpa		Q9yvj4 melanoplus	089744 buzura supp	Q9nj07 spodoptera	Q9u492 trichoplusi	09j827 spodoptera	Q9vem2 drosophila

ALIGNMENTS

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RESULT
Q9UNH1
           DRR REPRESENTATION OF THE PROPERTY OF THE PROP
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01-MAY-2000 (TrEMBLrel. 13, C:
01-MAY-2000 (TrEMBLrel. 13, L:
01-JUN-2001 (TrEMBLrel. 17, L:
APIZ-MLT FUSION PROTEIN.
Pfam: PF00653; BIR; 3.
Pfam: PF00047; 1g; 2.
SMART; SM00238; BIR; 3.
SMART; SM00115; CASC; 1.
SMART; SM00410; IG_1!ke; 1.
SMART; SM00410; IG_1!ke; 1.
SMART; SM00410; IG_1!ke; 1.
PROSITE; PS01282; BIR_REPEAT_1; 3.
PROSITE; PS01283; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDITINE=99272400; PubMed=10339464;

MEDITINE=99272400; PubMed=10339464;

Dierlamm J., Baens M., Wlodarska I., Stefanova-Ouzounova M.,

Hernandez J.M., Hossfeld D.K., De Wolf-Peeters C., Hagemeijer A.,

Van den Berghe H., Marynen P.;

"The apoptosis inhibitor gene API2 and a novel 18q gene, MLT, are
recurrently rearranged in the t(11:18)(q21:q21)p6ssociated with
mucosa-associated lymphoid tissue lymphomas.";

Blood 93:3601-3609(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UNH1
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InterPro; IPR003600;
InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                           ; IPR003576; Caspase.; IPR001369; ICE_p20.; IPR003598; Ig_C2.; IPR003600; Ig_like.; IPR003006; Ig_MHC.
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Last annotation update)
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Best Loc
Matches
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Best 1
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"Cloning and Characterization of the Rat Homologs
Apoptosis Protein 1, 2, and 3 Genes.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ dat
-: SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
InterPro; IPRO01370; BIR.
InterPro; IPRO01370; BIR.
InterPro; IPRO01315; CARD.
InterPro; IPRO01315; CARD.
InterPro; IPRO01841; Znf_ring.
Pfam; PF00653; BIR; 3
Pfam; PF00659; CARD; 1.
Pfam; PF00697; zf-C3HC4; 1.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00118; BIR; 3.
SMART; SM00118; BIR; 3.
PROSITE; PS0128; BIR; 3.
PROSITE; PS0128; BIR; 3.
PROSITE; PS0128; BIR, REPEAT_1; 1.
PROSITE; PS0128; BIR, REPEAT_1; 3.
PROSITE; PS0129; CARD; 1.
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                                                                                                                                                                                                                                        0902C6 PRELIMINARY; PRT; 589 AA. 9902C6; 9902C6; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 101-JUN-2001 (TrEMBLREL 17, Last annotation update) 11HIBITOR OF APOPTOSIS PROTEIN 2.
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Q9ESE9;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota: Metazoa: Chordata:
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=10116;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
INHIBITOR OF APOPTOSIS PROTEIN 1.
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Local S
                                  SSUE-KIDNEY;
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Local Similarity
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Rodentia;
      မှု
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; Pred. NO. 6.9e
1; Mismatches
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      Saikumar
                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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e_Rat Homologs of
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Best Local
Matches 5
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InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00619; CARD; 1.
Pfam; PF00619; CARD; 1.
Pfam; PF00619; ZfC3HC4; 1.
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InterPro; IPRO01315; CARD.
InterPro; IPR001841; Znf_rin.
InterPro; IPR001841; Znf_rin.
InterPro; IPR001841; Znf_rin.
InterPro; IPR001841; IR; 3.
Interpro; IR; 3.
INTER
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Q9ESE8;
Q1-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                     SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00114; CIRD; 1.
SMART; SM001184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1;
PROSITE; PS50143; BIR_REPEAT_2;
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.; "Cloning and Characterization of the Rat HomoLogs of the Apoptosis Protein 1, 2, and 3 Genes."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1;
PROSITE; PS50143; BIR_REPEAT_2;
PROSITE; PS50209; CARD; 1.
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-!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
EMBL; AF190020; AAF04585.1; -.
HSSP; Q13490; 1QBH.
                                                                                                                                                                                                                                                                                           Zinc-finger
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
HOLCIK M., Lefebvre C.A., Hicks K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 2.
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                                     1 CELYRMSTYSTFPAGVPVSERSLARAGFYYTGVNDKVKCFCCGLMLDNWKLGDSP
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CELYRMSTYSAFPRGVPVSERSLARAGFYYTGVNDKVKCFCCGLMLDNWKQGDSP
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                                                                                                                                Similarity 94.
52; Conservative
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52; Conserv
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; Pred. No. 5.3e
0; Mismatches
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0; Mismatches
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Sciurognathi; Muridae;
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No. 5
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.3e-29;
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Best Local Similarity
Matches 44; Conser
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Q9DDN2;
Q1-MAR-2001 (TrEMBLrel. 16, C:
Q1-MAR-2001 (TrEMBLrel. 17, L:
Q1-JUN-2001 (TrEMBLrel. 17, L:
APOPTOSIS INHIBITOR CH-TAP1 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O57319 PRELIMINARY; PRT; 610 AA.
O57319; O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 1 (IAP) (INHIBITOR OF T
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Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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"The apoptosis inhibitor ch-IAP1 is a direct transcriptional target
v-Rel and c-Rel.",
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF311289; AAG42316.1; -.
InterPro; IPR001370; BIR.
InterPro; IPR001370; BIR.
Pfam; pr00553; BIR; 3.
Pfam; pr00553; BIR; 3.
PROSITE; PS01282; BIR_REPEAT_1; 1.
PROSITE; PS01282; BIR_REPEAT_2; 3.
PROSITE; PS01343; BIR_REPEAT_2; 3.
PROSITE; PS01343; BIR_REPEAT_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-WHITE LECHON; TISSUE-EMBRYONIC FIBROBLAST;
MEDLINE-9803801; PubMed-9372964;
WEDLINE-98038801; PubMed-9372964;
You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
"ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
mediator of the antiapoptotic activity of the v-Rel oncoprotein.";
Mol. Cell. Biol. 17:7328-7341(1997),
-i- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Aves: Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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THESUB SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 AA;
         THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT
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, Last annotation
1 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                                                    AND AT VERY LOW
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                                                                         Matches
                                                                                                  Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00653; BIR; 3.
Pfam; PF00653; CARD; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00338; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1: 3
PROSITE; PS0143; BIR_REPEAT_2: 3
PROSITE; PS50143; BIR_REPEAT_2: 3
PROSITE; PS50209; CARD; 1.
Apoptosis; Zinc-finger; Repeat.
REPEAT 30 97
REPEAT 176 242
REPEAT 176 242
REPEAT 176 329
SEQUENCE 610 AA; 68924 MW; AD
                                                                                                                                                                                                                                                                                                                                                                                                    Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;

"Cloning and Characterization of the Rat Homologs of the
Apoptosis Protein 1, 2, and 3 Genes.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

EMBL; AF183429; AAG22969.1; --

InterPro; IPR001370; BIR.

InterPro; IPR001310; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ESFO PRELIMINARY; PRT; 496 AA.
Q9ESFO;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
INHIBITOR OF APOPTOSIS PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: MEMBER OF THE IAP FAMILY.
-!- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACU-APOPTOSIS PROTEIN REPEAT).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINCEMBL; AF008592; AAB88044.1; -.
HSSP; Q13499; LQBH.
                                                                                                                                                                                                    SMART; SM00238; BIR; 3.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1;
PROSITE; PS50143; BIR_REPEAT_2;
Zinc-finger.
SEQUENCE 496 AA; 56117 MW; 9
                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00653; BIR; 3.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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CELYRMSTFSTFPVNVPVSERRLARAGFYYTGVQDKVKCFSCGLVLDNWQPGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                         l Similarity
27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                            Conservative
                                                                                                                                                                                                          56117 MW; 9BEF142AAEC5B798 CRC64;
                                                                                               49.5%;
50.9%;
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BIR REPEAT 2.
BIR REPEAT 3.
BIR REPEAT 3.
C3HC4-TYPE.
C3HC4-TYPE.
MW; ADF47619650B44A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                         Score 152; DB Pred. No. 2.8e 8; Mismatches
                                                                               8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 247;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BACULOVIRAL
                                                                                                     DB 11;
..8e-11;
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                                                                                                                             Length 496;
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EFNRLKTFANFPSSSPVSASTLARAGFLYTGEGDTVQCFSCHAAVDRWQYGDS

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RESULT
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                           Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.

"Cloning, characterization and regulation of an inhibitor of apo
"T protein in the rat corpus luteum.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

'I SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

REMBL; AF304334; AAG41193.1; -.

REMBL; AF30434; AAG41193.1; -.

REMBL; AF304334; AAG41193.1; -.

REMBL; AF30434; AAG41193.1; -.

REMBL; AF304334; AAG41193.1; -.

REMBL; AF304334; AAG41193.1; -.

REMBL; AF30434; AAG41193.1; -.

REMBL; AF3044; AAG41193.1; -.

REMBL; AF3044; AAG41193.1; -.

REMBL; AF3044; AAG41193.1; -.

REMBL; AF3045; AAG41193.1; -.

REMBL; AF3045; AAG41193.1; -.

REMBL; AF3045; AAG41193.1; -.

REMBL; AF3045; AAG4193.1; -.

REMBL; AF3045; AAG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 27
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"Cloning, characterization and regulation of an inhibitor of apo
T protein in the rat corpus luteum.";
L Submilted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
C -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
REMBL, AF304333; AAG41192.1;
REMBL, AF304333; AAG41192.1;
REMBL, AF304533; AAG41192.1;
REMBL, AF90653; BIR;
RING-TYPE ZINC FINGER.
REMBL, AF90653; BIR; 3.
REMBL, SEMBL, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9EQ04 PRELIMINARY; PRT; 501 AA.
Q9EQ04;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota: Metazoa: Chordata;
Mammaila: Eutheria: Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01282; BIR REPEAT_1;
PROSITE; PS50143; BIR REPEAT_2;
Zinc-finger,
SEQUENCE 501 AA; 56548 MW; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9EQ05 PRELIMINARY; PRT; 501 AA.
09EQ05;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11-JUN-2001 (TrEMBLREL. 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FINELET FAME PSSSPVSASTLARAGE LYTGEGD TYQCF SCHAAVD RWQYGDS
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27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
   BIR_REPEAT_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56548 MW; 0973FBF28E81C5A0 CRC64;
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Pred. No. 2.8e-11;
8; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
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                                                                                                                                                                                                                                                                                                                                                                                               A.M.;
apoptosis
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL/
EMBL; AF250284; AAG02727.1; -.
InterPro; IPR001370; BIR.
InterPro; IPR001B41; Znf_ring.
Pfam; PF00653; BIR; 2.
SMART; SM00238; BIR; 2.
SMART; SM00238; BIR; 2.
SMART; SM00184; RING; 1.
PROSITE; PS50143; BIR_REPEAT_2; 2
SEQUENCE 264 AA; 30547 MW; 2E
                                            Q91A70 PRELIMINAKY; Q91A70; Q9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9EN27;
01-MAR-2001
01-MAR-2001
01-JUN-2001
AMV021.
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Viruses; dsDNA
Entomopoxvirus
Gallus.
NCBI_TaxID=9031;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete Genomic Sequence of the Amsacta moore; Analysis and Comparison with Other Poxviruses."; virology 274:120-139(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9EN27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=20396580; PubMed=10936094;
Bawden A.L., Glassberg K.J., Diggans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMV021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moyer R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moyer R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=28321;
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                                                                                                                                                                                                                                                                                                                                                      11
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27; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 49.0
25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entomopoxvirus (AmEPV).
viruses, no RNA stage; Poxviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.28;
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17,
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Last sequences
Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 145; DB 12;
Pred. No. 1.1e-10;
B; Mismatches 18;
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Pred. No. 2.8e-11;
8; Mismatches 18;
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Best Local Similarity 51.0
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 51.0
Matches 26; Conservative
  Q9YNL8;
Q9YNL8;
01-MAY-1999
01-MAY-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific genes.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ

EMBL; AF221083; AAF35320.1; -.

InterPro; IPR001370; BIR.

Pfam; PF00653; BIR; 2.

SMART; SM00238; BIR; 2.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11-JUN-2001 (TrEMBLrel. 15, Craniator)
11-JUN-2001 (TrEMBLrel. 15, Craniator)
11-JUN-2001 (TrEMBLrel. 15, Created)
11-JUN-2001 (TrEMBLrel. 15, Last sequence update)
11-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11-JUN-2001 (TrEMBLrel. 17, Last annot
                                                                                                                                                                                                                                                                                                                                                               STRAIN-BREED FAYOUMI; TISSUE-SPLEEN, Zhou H., Lamont S.J.;
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SMART; SM00238; BIR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific genes.";
Submitted (JAN-2000) to the
EMBL; AF221082; AAF35319.1;
InterPro: IPR001370; BIR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BREED LEGHORN; TISSUE-SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Genetic variation among chicken lines and mammalian species
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                                                                                                                                                                                                        RMSTYSTFPAGVPVSERSLARAGFYYTGVNDKVKCFCCGLMLDNWKLGDSP
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                                                                                                                                                                                   RVKTFINWPTRIPVQPEQLADAGFYYVGRNDDVKCFCCDGGLRCWESGDDP 170
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197
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  (TrEMBLrel. 10, (TrEMBLrel. 10, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                PRELIMINARY;
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22602 MW;
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22347 MW;
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51.0%;
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Created)
Last sequence up
Last annotation
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Pred. No. 1.5e
5; Mismatches
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                                                                                                                                                                                                                                                             Score 143; DB 13;
Pred. No. 1.5e-10;
5; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                                                                 D7923DABCF623E1A CRC64;
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No. 1.5e-10;
ismatches 20;
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Q9R015
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                                                                                                       Query Match
Best Local S
Matches 25
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                                                                                                                                                                                                                                                                           HSSP; Q13490; 1QBH.

MGD; MGI:1398220; Bircle.

InterPro; IPR001370; BIR.

Pfam; PF00653; BIR; 3.

SMART; SM00238; BIR; 3.

PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.

PROSITE; PS50143; BIR_REPEAT_2; 3.

SEQUENCE 597 AA; 68322 MW; 4042E36E51A7F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00653; BIR; 2.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00238; BIR; 2.
SMART; SM00184; RING; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; UN
PROSITE; PS50143; BIR_REPEAT_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9R015 PRELIMINARY; PRT; 59/ AA.
Q9R015, 13/ Created)
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NEURONAL APOPTOSIS INHIBITORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99431676; PubMed=10501978;
Huang S., Scharf J.M., Growney J.D.,
"The mouse Naip gene cluster on Chror
functional transcripts.";
Mamm. Genome 10:1032-1035(1999).
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TaxID-10448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIRCLE OR NAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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HSSP; Q13490; 1QBH.
InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF135493; AAD56765.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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IAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 EAARLRIFIEWPRGLKQRPEKLAENGFFYTGRSDKVKCFYCDGGLDNWEQDDEP 177
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                                      N
ELYRMSTYSTFPAGVPVSERSLARAGFYYTGVNDKVKCFCCGLMLDNWKLGDSP
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                                                                                                          . Similarity 46.3
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Similarity
26; Conserv
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Znf_ring.
                                                                                                                                             43.6%;
                                                                                                       Score 134; DB 1
Pred. No. 6.9e-0
6; Mismatches
                                                                                                          6;
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Pred. No. 5.3e-10;
8; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                          4042E36E51A7F9A0
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2.
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mosome 13
                                                                                                   3 11;
--09;
23;
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                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                           Length
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232 EELRMDMFKDWPQESPVGVEALVRAGFFYTGKKDIVRCFSCGGCLEKWAEGDDP 285

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RESULT 15
088642
ID 088642
AC 086642
DT 01-NOV
DT 01-NOV
DT 01-JUN
DE INHIBI
GN RIAPL
OS RATLUS
OC EUKARY
OC MAMMAL
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DR INTERP
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DR HSSP;
DR HSSP;
DR SMARF;
DR SMARF;
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SEQUENCE FROM N.A.

STRAIN-WISTAR; TISSUE-OVARY, CORPUS LUTEUM;

RR STRAIN-WISTAR; TISSUE-OVARY, CORPUS LUTEUM;

RR STRAIN-WISTAR; TISSUE-OVARY, CORPUS LUTEUM;

RT Cloning and characterisation of an inhibitor of apoptosis protein at the corpus luteum.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

REMBL; AF081503; AAC32497.1; -.

REMBL; AF081503; AAC32497.1; -.

REMBL; AF081503; ABC32497.1; -.

REMBL; AF081503; BIR: 2.

REMBL; AF081503; BIR: 2.

REMBL; AF081503; BIR: 2.

REASTTE; PS50143; BIR: 2.

RON_TER 21

RON_TER 224

RON_TE
                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.7%; Score 131; DB 11; Best Local Similarity 51.0%; Pred. No. 5.9e-09; Matches 26; Conservative 4; Mismatches 21;
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088642;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                  224
25209 MW; 213A52534D5EB56A CRC64;
                                      7,
                                      2002, 16:03:53
                                                                                                                                                                                                                                                                                                                                                                          21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 224;
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